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## RAW SEQUENCE LISTING

DATE: 09/17/2004

PATENT APPLICATION: US/10/723,872

TIME: 09:08:32

Input Set : N:\Crf3\RULE60\10723872.raw.txt

Output Set: N:\CRF4\09172004\J723872.raw

## SEQUENCE LISTING

## 1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Holmes, Stephen D.  
 3 Gross, Mitchell S.  
 4 Sylvester, Daniel R.

5 (ii) TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
 6 Treatment of IL4 Mediated Disorders

7 (iii) NUMBER OF SEQUENCES: 58

8 (iv) CORRESPONDENCE ADDRESS:

9 (A) ADDRESSEE: SmithKline Beecham Corporation

10 (B) STREET: Corporate Intellectual Property, UW2220 - 709  
 11 Swedeland Rd.

12 (C) CITY: King of Prussia

13 (D) STATE: PA

14 (E) COUNTRY: USA

15 (F) ZIP: 19406-2799

16 (v) COMPUTER READABLE FORM:

17 (A) MEDIUM TYPE: Floppy disk

18 (B) COMPUTER: IBM PC compatible

19 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

21 (vi) CURRENT APPLICATION DATA:

C--> 22 (A) APPLICATION NUMBER: US/10/723,872

C--> 23 (B) FILING DATE: 26-Nov-2003

24 (C) CLASSIFICATION:

25 (vii) PRIOR APPLICATION DATA:

W--> 26 (A) APPLICATION NUMBER: US/09/879,461

27 (B) FILING DATE: 12-Jun-2001

W--> 28 (A) APPLICATION NUMBER: 08/612,929

29 (B) FILING DATE:

W--> 30 (A) APPLICATION NUMBER: US 08/136,783

31 (B) FILING DATE: 14-OCT-1993

32 (viii) ATTORNEY/AGENT INFORMATION:

33 (A) NAME: Sutton, Jeffrey A.

34 (B) REGISTRATION NUMBER: 34,028

35 (C) REFERENCE/DOCKET NUMBER: P50186-2

36 (ix) TELECOMMUNICATION INFORMATION:

37 (A) TELEPHONE: (215) 270-5024

38 (B) TELEFAX: (215) 270-5090

39 (2) INFORMATION FOR SEQ ID NO: 1:

40 (i) SEQUENCE CHARACTERISTICS:

41 (A) LENGTH: 396 base pairs

42 (B) TYPE: nucleic acid

ENTERED

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43         (C) STRANDEDNESS: double
44         (D) TOPOLOGY: unknown
45     (ii) MOLECULE TYPE: cDNA
46     (ix) FEATURE:
47         (A) NAME/KEY: CDS
48         (B) LOCATION: 1..396
49     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
50     ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTG CTC TGG GTT CCA      48
51     Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Trp Val Pro
52         1             5             10             15
53     GGC TCC ACT GGT GAC ATT GTG CTG ACC CAA TCT CCA GCT TCT TTG GCT      96
54     Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
55         20             25             30
56     GTG TCT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC AGC CAA AGT      144
57     Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
58         35             40             45
59     GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA      192
60     Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
61         50             55             60
62     GGA CAG CCA CCC AAA CTC CTC ATC TAT GCT GCA TCC AAT CTA GAA TCT      240
63     Gly Gln Pro Pro Lys Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
64         65             70             75             80
65     GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC      288
66     Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
67         85             90             95
68     CTC AAC ATC CAT CCT GTG GAG GAG GAG GAT GCT GCA ACC TAT TAC TGT      336
69     Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
70         100            105            110
71     CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GGC ACC AAG CTG      384
72     Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
73         115            120            125
74     GAA ATC AAA CGG
75     Glu Ile Lys Arg
76         130
78 (2) INFORMATION FOR SEQ ID NO: 2:
79     (i) SEQUENCE CHARACTERISTICS:
80         (A) LENGTH: 132 amino acids
81         (B) TYPE: amino acid
82         (D) TOPOLOGY: linear
83     (ii) MOLECULE TYPE: protein
84     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
85     Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
86         1             5             10             15
87     Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
88         20             25             30
89     Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
90         35             40             45
91     Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
92         50             55             60

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93   Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
94     65              70              75              80
95   Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
96                85              90              95
97   Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
98                100             105             110
99   Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
100              115             120             125
101   Glu Ile Lys Arg
102     130
104 (2) INFORMATION FOR SEQ ID NO: 3:
105   (i) SEQUENCE CHARACTERISTICS:
106       (A) LENGTH: 483 base pairs
107       (B) TYPE: nucleic acid
108       (C) STRANDEDNESS: double
109       (D) TOPOLOGY: unknown
110   (ii) MOLECULE TYPE: cDNA
111   (ix) FEATURE:
112       (A) NAME/KEY: CDS
113       (B) LOCATION: 64..483
114   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
115   GAATTTCGCGG CCGCTATGCA GGGACAATCA GCAGCAGCAA TGAGGAAGTA AGCCTGTGCA      60
116   GAT ATG AAC AGG CTT ACT TCC TCA TTG CTG CTG CTG ATT GTC CCT GCA      108
117     Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Ile Val Pro Ala
118       1              5              10              15
119   TAT GTC CTG TCC CAG GTT ACT CTG AAA GAG TCT GGC CCT GGG ATA TTG      156
120   Tyr Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu
121                20              25              30
122   CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA      204
123   Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser
124                35              40              45
125   CTG AGC ACT TCT GGT ATG GGT GTG AGC TGG ATT CGT CAG CCT TCA GGA      252
126   Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly
127       50              55              60
128   AAG GGT CTG GAG TGG CTG GCA CAC ATT TAC TGG GAT GAT GAC AAG CGC      300
129   Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg
130     65              70              75
131   TAT AAC CCA TCC CTG AAG AGC CGG CTC ACA ATC TCC AAG GAT ACC TCC      348
132   Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
133     80              85              90              95
134   AGC AAC CAG GTA TTC CTC AAG ATC ACC AGT GTG GAC ACT GCA GAT ACT      396
135   Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr
136                100             105             110
137   GCC ACA TAC TAC TGT GCT CGA AGA GAG ACT GTG TTC TAC TGG TAC TTC      444
138   Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe
139                115             120             125
140   GAT GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC TCA
141   Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
142     130              135              140

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144 (2) INFORMATION FOR SEQ ID NO: 4:
145   (i) SEQUENCE CHARACTERISTICS:
146       (A) LENGTH: 140 amino acids
147       (B) TYPE: amino acid
148       (D) TOPOLOGY: linear
149   (ii) MOLECULE TYPE: protein
150   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
151   Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Ile Val Pro Ala Tyr
152       1             5             10             15
153   Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
154       20             25             30
155   Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
156       35             40             45
157   Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
158       50             55             60
159   Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
160       65             70             75             80
161   Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser
162       85             90             95
163   Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala
164       100            105            110
165   Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp
166       115            120            125
167   Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
168       130            135            140
170 (2) INFORMATION FOR SEQ ID NO: 5:
171   (i) SEQUENCE CHARACTERISTICS:
172       (A) LENGTH: 60 base pairs
173       (B) TYPE: nucleic acid
174       (C) STRANDEDNESS: double
175       (D) TOPOLOGY: unknown
176   (ii) MOLECULE TYPE: cDNA
177   (ix) FEATURE:
178       (A) NAME/KEY: CDS
179       (B) LOCATION: 1..60
180   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
181   ATG GTG TTG CAG ACC CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT      48
182   Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
183       1             5             10             15
184   GGT GCC TAC GGG
185   Gly Ala Tyr Gly
186       20
188 (2) INFORMATION FOR SEQ ID NO: 6:
189   (i) SEQUENCE CHARACTERISTICS:
190       (A) LENGTH: 20 amino acids
191       (B) TYPE: amino acid
192       (D) TOPOLOGY: linear
193   (ii) MOLECULE TYPE: protein
194   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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195      Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
196      1                      5                      10                      15
197      Gly Ala Tyr Gly
198      20
200 (2) INFORMATION FOR SEQ ID NO: 7:
201      (i) SEQUENCE CHARACTERISTICS:
202          (A) LENGTH: 57 base pairs
203          (B) TYPE: nucleic acid
204          (C) STRANDEDNESS: double
205          (D) TOPOLOGY: unknown
206      (ii) MOLECULE TYPE: cDNA
207      (ix) FEATURE:
208          (A) NAME/KEY: CDS
209          (B) LOCATION: 1..57
210      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
211      ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT      48
212      Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
213      1                      5                      10                      15
214      GTC CAC TCC
215      Val His Ser      57
217 (2) INFORMATION FOR SEQ ID NO: 8:
218      (i) SEQUENCE CHARACTERISTICS:
219          (A) LENGTH: 19 amino acids
220          (B) TYPE: amino acid
221          (D) TOPOLOGY: linear
222      (ii) MOLECULE TYPE: protein
223      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
224      Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
225      1                      5                      10                      15
226      Val His Ser
228 (2) INFORMATION FOR SEQ ID NO: 9:
229      (i) SEQUENCE CHARACTERISTICS:
230          (A) LENGTH: 423 base pairs
231          (B) TYPE: nucleic acid
232          (C) STRANDEDNESS: double
233          (D) TOPOLOGY: unknown
234      (ii) MOLECULE TYPE: cDNA
235      (ix) FEATURE:
236          (A) NAME/KEY: CDS
237          (B) LOCATION: 1..423
238      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
239      ATG GTG TTG CAG ACC CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT      48
240      Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
241      1                      5                      10                      15
242      GGT GCC TAC GGG CAG GTT ACC CTG AAA GAG TCT GGC CCT GGG ATA TTG
243      Gly Ala Tyr Gly Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu      96
244      20                      25                      30
245      CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA
246      Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser      144

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**VERIFICATION SUMMARY**

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Input Set : N:\Crf3\RULE60\10723872.raw.txt

Output Set: N:\CRF4\09172004\J723872.raw

L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:28 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)  
L:30 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)